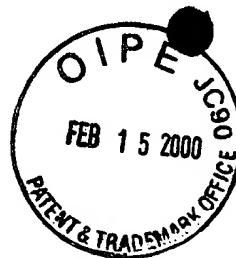


SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Lavi, Sara

(ii) TITLE OF INVENTION: MANIPULATION AND DETECTION OF PROTEIN
PHOSPHATASE 2C -PP2CALPHA- EXPRESSION IN TUMOR CELLS FOR
CANCER THERAPY, PREVENTION AND DETECTION

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Kohn & Associates
- (B) STREET: 30500 Northwestern Hwy.
- (C) CITY: Farmington Hills
- (D) STATE: Michigan
- (E) COUNTRY: US
- (F) ZIP: 48334

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kohn, Kenneth I.
- (B) REGISTRATION NUMBER: 30,955
- (C) REFERENCE/DOCKET NUMBER: 2290.00037

(ix) TELECOMMUNICATION INFORMATION:

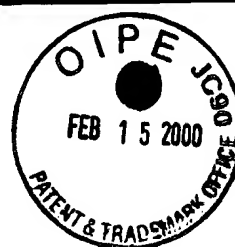
- (A) TELEPHONE: (810) 539-5050
- (B) TELEFAX: (810) 539-5055

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asn Asp Asp Thr Asp Ser Ala Ser Thr Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asn Lys Asp Asn Asp Gly Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGATCAAGT CATAATGGGA

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTGGAGTCT GATTTACAAC

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAAGTAGTCG ACACCTGT

18

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTTGAGACC TTCAACACCC C

21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGGCCATCT CTTGCTCGAA GTC

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Ala Phe Leu Asp

1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGATCCGC ATGGGAGCAT TTTTAGAC

28

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Asp Asp Met Trp
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGATCCT TACCACATAT CATCAGT

27

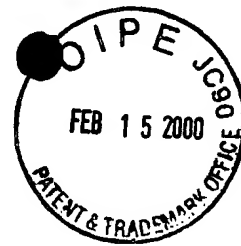
(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Silencer Region"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTCCATCAC TAGGGGTTCC TGGAGGGGTG GAGTCGTGAC GTGAATTACG TCATAGGGTT
60

AGGG

64

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Mini-silencer region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTCCCATCA CTAGGGGTTC CT

22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "35-3.seg (Figure 3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTTGTC A AATTACTAT TCAGTGTGAT TTTAGTGGA TGAAACCTCA TGACTAGTAT
60

ATTATGACAT TAGCTTTGCG TAGTGAAGGC ACAAGCTGCT AAGTGGTTAG GGATGTATT
120

TGCCGTAGCC TGTATCACNC CAGGTCCTGG GCTCGGTTCC TAGCATTACA GGAAAAAGCA
180

GGCGGTGGTT GACCTTTAAT GAATGGATTT TTCAATTTAG AAGTTGGTTT CATTTTAAAG
240

AATTCAAAAA TGTTCCCAT AGCACTTTGT TTTGACATTG AGATCAGCTG CTAATTGAGG
300

TCCAGTATAT ACTTAGAAAA CTGAGCGAAA CTTTGATGGA CACACACACA CACCCCTGTT
360

GTTCAATTAA TAATTGAACT AAATAAAATA CTGTTTAGTC ATCCACGTAA GCAAGAGGCC
420

TGTGTAAACA GTATTTGTAT TAGTAAAAAC TTTATAACAT AGTTACATAA TCAGCATCAT
480

TTTTTTTATG GACCTTATAG TTGGCTACTT CACTGGGTTT GTTATAATTT AATCAGACTC
540

CTAAATAGGT TAAATTTCTG AATTGCCTAC TTCAGTTTGT AAGAATTATT TTGTTTCATA
600

ATTTCCCATG CATATCTGGT AAATAATTCT GGATTGTTTC TAAAGGGGAG AGCAAGGTCT
660

CTTATGCAAA GTGAAAATCT AGATATGCTG TTTGTAAGAA TATAATAGTG ATAAAGTAGT
720

GTCCTTTTGC TCAGTGCCTC CATTCTTACC AGGCTGTGAC TGATCTTCAG TATTATTGAG
780

ACAGTCACTA TTAATATATC CGTTGCACAG TGGGGAAATT GAGGGAAGTT AGATAGGCAT
840

CGGGTATCTT AATCATAACT CACATATACC CAGCTGGCTA GTCAGCCTAG CTAAGACAGT
900

TCACACCCAG TTGAGGCAGC TTGCTGTTGG CCATTAGTAG GTAACCTAAT GGCTTGGTTT
960

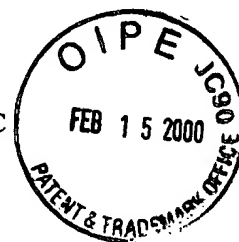
CTTCACTGGT AAGGTGGGGA TATAATAATG CCAATAATTG CATAATGATT AAAGACATTA
1020

ATATATTCCA TAAAATTTCC TGAATAGTGC TTAGCTGGTA CCCCTCCCCA CACATGCACC
1080

CCAGTCCAAT GTTCAGATGT TTAATTTGTT AAGCCCAGTT AATCCATTCC CCCTAATATC
1140

TTCTCCAGT TTGAAGAANG TTGAAGAATG TTGGGCTTGT TAGTTTAATT TTTAAGAAG
1200

CATATCATGT TGCTTTTTTA AAACATGTTT CTTTGGGTTT TGGCTTCCCC TTTTGGAAAG
1260



AATTCCAATT TACACTTATG GAAGAAAGCC ATTGTCCCCT CCAATTTCCC CCCCTGTCCC
1320

TTTCCAATAC AGCCCAACTC CCCATGTTTT GACTTCCTCC CCTGAACCAC CCCGTTCTCC
1380

TGTTTTTCCC TCCCCANAA AAAAAACCCA ATAATTTGAC TTTGGTAATT GAATTTCCCG
1440

CCNGTTAGGC NCCTGAATTG CCGAAATAAT TCCCCGTGC NCCCNGGANT TTTGGCACCC
1500

CCTGCCCCTT AACCTGTTCT GCTGCCCCC ATTTTAAAT GGCTTGCCGC NTTACNCCAA
1560

ANACTGCCTT TCC

1573

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "35-T7.seg (Figure 3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCGATCTCA CAAAGTCACA GAGCTCTTCG TTTCCCATGA CATCCAGAT ACCATCACAT
60

GCAAGAATAA TGAAGTATC GTCCTCTTCA GACCTTTCAA TATCATGGAC TTCTGGCTCT
120

GGTGAGACGA GCTGCTCTGT GGGACCTTTT CCATGGACAC ATTTGTAATC GAAATCCCCA
180

AGGGCCCTTG ACACAGCCAG AGAGCCATTT ACACGCTGAA TCATCACAGA GCCCCCTGCA
240

TTCTGAATTC GTTCTTTTTC CAGCGGGTTA CTTGGTTTGT GGTCTTGTGT GAAGAAGTGA
300

ACTTTCCTGT TTCTACAAAG CAAACCTCTC GAGTCTCCAC AGTTAATGAA GTAAGTATGT
360

TTGGGGAGAA ATTAAGACCC CCACAGCTGT TTGACCCACT TCCTATCTGC ACCATGTTTT
420

CCTTCCTCCT GACATGACTC CTCATGTTGT TTCCATCAAT CTCCCAGAAA AACCTGTTCC
480

TGATCCCCAT TCCTTTACAT TTTCCACAG AAAGGTGCTC CCTGCAGAGC CTTTAAAAT
540

CCCTGGTTTA TTGGTGATGT TGATTCTNAA CAAATGCTCC ACAGCCAGTA TTTNGGCAAC
600

CTTGAAAAAC CAGCATGCCC ATCCATATAC AGCCAAGAAT GACCATGTTC TCCAGTTCCA
660

CTTTNGGCAA ACCCAATCCA CAGCCGTTNT GCGCATCCTC CCATTTC AAC TCCGCCCAAC
720

CNTTGCNTGC TGCNTTAAGC CATATCGCAA CCCATCCCCC CTGCCCCCTG GGGCATTATG
780

CNTTTCATC TTTGGTTGTC TAAAATGCTC CCATTATGAC TTGATCCTCT AGGTCTGCAA
840

AGGAAGAGAA ATAAGAAAGT TAGTAACTGT CTTTGAAACA AAGCACACAT CCAACAGTCT
900

TTTTGAAGCA CCTACGAGAT ACAAGGAAAC GTAAAACTC ATAGGCTATA GCCATAAGCA
960

TTGTTCTACT GACTTGGAAT ATGTAGAGAT TAATAAGAAA GGGAAAGGCT GATCAAGTAC
1020

AGCTCAACCA GACAAGCAGC AGATGGAAC AAGTCACCAG GTAAAAGAGA GCTTGTTTGC
1080

CTCTCTGTGA TACCAAGGAG GCCCAGCAGT GACCATTAAC TTACATGAAC TAGGCAAGAT
1140

TTCAGGGTGC ATTCATCATA TGTAACCTCT CAATTAAGTT GTGTGTTGAT TAAAAAAAT
1200

AATTCATAGA AACATACAAG TATCTACTAC TTCAGGGAAC CTTAGCTAAG TACTCAGGAA
1260

TGTTGAGAGT TTGATTCCAT GCTATTTAGT TTTGTTTCTA CAACTAGATA CCTTTGGTAA
1320

AAATAAAAAG TAATTACTCA CACTGGTCCA AATTTTCAGT GCCTTGTGCA GGTCAATTCTC
1380

TTTAGCTGGA ATTCCCTGCC TCACCTCTTT ACCAACAGAA AAAAAATACA CCTGTTTCTA
1440

TCCTTTGAAA TCCAGTTCAA TTGTTCCCCC TTCCTCCAGA CTTTACAGTC CTTGAAAAAA
1500

ACAAGTTATT AACTACAGAA GTCAGCTTCC ATTTCCAGTT NGGAATGTTT TTTAATGAAC
1560

AATTTTATTG TTCNAAATCT NACNATATGA TAACTAANCN AATGGTAATA ATATTTTCAN
1620

CCCTGCCCTA TGGCCGCTNT TTTAATCCT NAAAAAAATC NAAGGTCTAT TCCNCCCNC
1680

CTTGCCAATA CTTNACANCN CCAGTTCCT GATCTGGAAT GGACCCACAA AGGTCAAGAC
1740

TTAGGTTANC CCTTGCTCAC AACTAAAGA AAATCTTAAA GGAGAACAGA ATACTGAAGA
1800

GAGAAATGAG GGTGAAGGAC AGTGTTGAGG TGACGTTCTG AAACCAGGGG ACTAAANATA
1860

CCANAANTGG TGTNCAGAC AGAAATGGTA TGGAAAATC CTTAGGAAAG AAATGACANN
1920

TNTTGTTTCG CAGCAACCCC CNCACATGGC TTTCTCTTT TCCTTCTGCT GATTAAGTGA
1980

TGCACNTGGT ANAAAAGTCA ACANACCCCT CCTCCACNCA GACTCCCACC GAGTACANN
2040

GCCCATGTGC TCANTACACT CTGCCCCAAA CTCNNANNAT TCATTCNNCT CCCCNTGTNA
2100

TTTATNAGGG CCTTCCCNT CAGTTNTCTN ATCNCCAACG GANATTANCC TTCCANNAT
2160

TTACCCCCNN TTTGTACANC ACATNNTGGC NNGTGCCACN GTTANGCGTC GGCNTCCCTG
2220

TTNCACTNCA TCCCTCATCN TTAGGCCANG TTTGATTCTC CNGTGCANAN TTTCCGCANN
2280

ANCNTACCCC TTGCACCNTC CATNTCTNNG GAANAACCTC CGGTTCTGAA TCTNCCCCNN
2340

TCCCGTCNCT CCCCNTTCT TTCTTTTCTC TANTTTTTC CNNGGNACGG GTTGNGGTNA
2400

ATNAANNCCC CTCCTTCGTC TATTCANCCC TTCCTATGNA CACTTCCTGN CCCCCTATCT
2460

CTCTATNTNC TNCTCTCTAT ATCTNNATCC CNTCTTCNCN TGCCNCTCCC TNGTNTTNA
2520

NCGGGTATTT NTTNTTCTCC TCNTCTTCTT CCCCTNTNTA NCCNTNCTNC NNNCNNNCCC
2580

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "5H-1 (Example 10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGGGAGAG GACTGAAATA TTTCCACAGC CTTTTTATTG GTGGTGATGG TAGTGATGGT
60
TAGGATTCTT TCTTCTTTC TTTCTTCTT TCTTCTTTC TTTCTTTTTT TTTTTTTTTT 120
TTTTTTTTTT GAGACAGGGT TTCTCTGGGT ACTCCTGGAA CTCACCTTGT GGACCATGAA
180
TGACATGAAT ACTTCGATAT ATACATACAT ACAAAGACAC ATATTTTAA AAAGAGAATT
240
AGAGTAGAGC TGGGGCAATT GTGGAACACA CCTTAACT CAGGCAGATT TCTGCGTTCA
300
AGGTCACCTT GGATTACAAG GCAGCTAGGG CTACACAGAG AAACCATATC TCAAAAAAAAA
360
GAAAAAATAA TGAAAGAAAG AAAGGAAGGA AGGAAGGAAG GAAGGAAGGA
AGGAAGGAAG 420
AAAGGAAGGT AGGAAGAAAG GTATTTTCCT AAAAAAAAAA AAAAAAAAAA TTTATTCCGG
480
GCAGTGGTGG CAAATGCTTT TAATCCCACC ATTTGGGAAA GCAGAGGCAG ACAGATTAAA
540
TTTTCAAGGC CCACCTGGTC CTACACAGTG AATTCAGGA ACACCTAGGT TTACCCANAA
600
AAAACCCCC CTTGAAATAA AAAAAATAA ATTAAATAA TAAAATTAA AAATAAAACC
660
CGGGCGTTAA ACCCNCTTTT ATCCCCCAC TTNGGAAGCA AAAGCCGGCN GATTCTGAA
720
TTCNAGGCCN CCCTGTCTAT GAATTANTTC CCNGAACACC CNAATTTTTC NAAAAACCC
780

CCNTTCTTA AAAAANCCAA ATTATTATTN ATTAATTAAA TNAAATTACC

830

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "AN8T7 (Example 10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGTCCAAC AATGGTTTCC ACTTGTCTGG CGGCCGCTCT AGAGTTTCCC ATAAGCTGGA
60

CTGAGAGATG GTGTGATTGC TGTGGGTGAC AAAGACAGAG GCACCTTTCA TCTCTACCCT
120

TCTCTTGTTT TGTTGTTTGT TTGAGACCGG TTCCCACTAT GTAGACCAGG CTGGAGGACA
180

GGGTCTCACT ATGTAGACCA GGCTGGCCTT GAACTCAAAG ACATCTGCCT GCCTCTGCCT
240

CCTGAGGGCT GGGATTAAAG GCGTGTGCTG CCACTGACAG CTTCTATCCT CCTGTCATCA
300

GTCCCGGCTC ACAGGGCCAG AAGATCTCTT CTATGCTTCC ACTATTTCCC CAATCCATTC
360

CCACGGCAGC CTCTCCATCT CCCTACCACC AAGACAGCAG CCTAGTGATA TAACAAAAC
420

TTTATTCACA GGAAACCGGA AAACAAAATC ACAACCAATC ATTTCTATCT AGTCCCTGCC
480

CTAGCCCTCC CTCCAAGCCC CTACATATCC TCCATCTGAG GGGGATGCAT GCGTTGGGTG
540

GGAGCTGCCG GCATCCTTAT CCTGGTTCCT GGAGTAGNGA AGAGTGGTTC TTTTCAACGN
600

CTAGGGNNCT CCCCTCCAAG TTNGGACCTC TCTTCCCAGG NCTTCNCCCC TCCCTNACAG
660

GGNACAAAAA ACCAGGNACG GCACNACGCC AGGNAGGAAG GGA CTCTTGG NAATGTTGGG
720

CAGGACTTGT CCTCAGAATT CCNNGGAGGA ATCAAGGGCC TTGAATTCGG GAACCACTNC
780

CGAGGNCTTC ANCANGGCAN AGTTCAATTT TCCATCCCGG TTGGCCCANC CTGGCCNG
838

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "CHINT (TABLE 5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGTGCCGGT CAAGGAACTG AACGTGCGAT TCCGGGACAG GCTACCCACT CCGATCCCAG
60

GAGAAGTTGT CATGGTGAGG GCCACCCTAG GTCTCTGCCC CTGCTGTGTC CCCCATCTTA
120

CCCATCCAGT AGGATCTAGA GGCTGTCGCC CCCTTGTTGA ATGCACAGAA GTCACAAGCG
180

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "HUMMDB (TABLE 5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCACCTCC GCCCTGTTTC GTCCAGGTCC TCCGGGTCAG GCTACCCCCG TCGCCGCCAG
60

AGCGCGGGGG AGGGGAGAGC TTCCTTTGTC TCCTATGCCT CCTCCCCCA TCCCGGCTCT
120

CCTGCGGGCA AGCGCCGAGG GGACACCGGG GAGTACCCCA CCTGAACCTC TGGGG
175

